Amendments to the Claims

Please amend claims 1-3, 11, 12, 18-21, 25, and 26 as indicated in the listing of claims.

The listing of claims will replace all prior versions, and listings of claims in the application.

Listing of Claims:

1. (Currently Amended) A method for detecting the presence of a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence in a neoplasm and the mammalian target neoplastic nucleic acid having the same mutant nucleotide sequence in a tumor margin tissue specimen comprising: [[,]]

extracting [~~the~~] nucleic acid present in the neoplasm and in the tumor margin tissue specimen, wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen is histologically normal; and

detecting the mutant nucleotide sequence in the nucleic acid extracted from the neoplasm and in the nucleic acid extracted from the tissue specimen, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm and the tumor margin tissue.

2. (Currently Amended) The method of claim 1, further comprising, prior to detecting the mutant nucleotide sequence, amplifying the nucleic acid extracted from the tissue specimen to produce an amplified nucleic acid, wherein [~~said~~] the detecting comprises detecting the presence of the mutant nucleotide sequence in the amplified nucleic acid.

3. (Currently Amended) The method of claim 2, wherein [~~said~~] the amplifying is by means of oligonucleotides that hybridize to flanking regions of the mutant nucleotide sequence.

4. (Previously Presented) The method of claim 1, wherein the mutant nucleotide sequence contains a mutation selected from the group consisting of a restriction fragment length polymorphism, a nucleic acid deletion, and a nucleic acid substitution.

Claims 5- 6. (Canceled).

7. (Previously presented) The method of claim 1, wherein the neoplasm is a neoplasm of the head or a neoplasm of the neck.

8. (Previously presented) The method of claim 1, wherein the neoplasm is head and neck cancer.

9. (Previously presented) The method of claim 1, wherein the neoplasm is a benign neoplasm.

10. (Previously presented) The method of claim 1, wherein the neoplasm is a malignant neoplasm.

11. (Currently Amended) The method of claim 2, further comprising, prior to detecting the mutant nucleotide sequence, cloning the amplified nucleic acid, wherein [~~said~~] the detecting comprises detecting the presence of the mutant nucleotide sequence in the amplified nucleic acid.

12. (Currently Amended) A method for detecting metastases in a subject having an excised tumor, the method comprising:

a) isolating tissue from a surgical margin adjacent to the excised tumor, wherein the tissue is histologically normal;

b) contacting the tissue from the surgical margin with an oligonucleotide that specifically hybridizes to a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm; and

c) detecting [~~the presence of~~] the mutant nucleotide sequence, when present in the tissue from the surgical margin, wherein the presence of the mutant nucleotide sequence in the tissue from the surgical margin is indicative of metastases.

13. (Canceled).

14. (Previously presented) The method according to claim 12 wherein the tissue is normal under a microscope.

Claims 15- 17. (Canceled).

18. (Currently Amended) A method for detecting a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence in a tissue specimen which is external to a primary neoplasm, comprising isolating a tissue specimen wherein the tissue specimen is histologically normal, extracting nucleic acid present in the tissue specimen to obtain extracted nucleic acid, and detecting the presence of the mutant nucleotide sequence in the extracted nucleic acid and in the tissue specimen, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm and in the tissue specimen.

19. (Currently Amended) A method for detecting a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence in a tumor margin tissue specimen which is external to a primary neoplasm, comprising isolating a tumor margin tissue specimen wherein the tissue specimen appears histologically normal, extracting nucleic acid present in the tissue specimen to obtain extracted nucleic acid, and detecting the presence of the mutant nucleotide sequence in the extracted nucleic acid, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm and in the tumor margin tissue.

20. (Currently Amended) A method for detecting the presence of a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence in a neoplasm and the mammalian

target neoplastic nucleic acid having the same mutant nucleotide sequence in a lymph node tissue specimen, comprising:

isolating a lymph node tissue specimen wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen appears histologically normal;

extracting nucleic acid present in the neoplasm and in the tissue specimen and, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm;

and detecting the mutant nucleotide sequence in the extracted nucleic acid from the neoplasm and in the extracted nucleic acid from the tissue specimen, when present in the tissue specimen.

21. (Currently Amended) The method of claim 20, further comprising, prior to detecting the mutant nucleotide sequence, amplifying the extracted nucleic acid from the tissue specimen to produce an amplified nucleic acid, wherein [~~said~~] the detecting comprises detecting the presence of the mutant nucleotide sequence in the amplified nucleic acid.

22. (Previously Presented) The method of claim 20, wherein the mutant nucleotide sequence contains a mutation selected from the group consisting of a restriction fragment length polymorphism, a nucleic acid deletion, and a nucleic acid substitution.

23. (Canceled).

24. (Previously presented) The method of claim 20, wherein the neoplasm is a neoplasm of the head or a neoplasm of the neck.

25. (Currently Amended) A method for detecting metastases in a subject having an excised tumor, the method comprising:

a) isolating tissue from a lymph node, which is external to a primary neoplasm, and wherein the tissue appears histologically normal;

b) contacting the tissue with an oligonucleotide that specifically hybridizes to a mammalian target neoplastic nucleic acid having a mutant nucleotide sequence, wherein the target neoplastic nucleic acid is selected from APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the mutant nucleotide sequence is present in the primary neoplasm; and

c) detecting the presence of the mutant nucleotide sequence in the tissue from the lymph node, wherein the presence of the mutant nucleotide sequence in the tissue from the lymph node indicates metastases.

26. (Currently Amended) The method of claim 25, wherein no more than an average of about one out of every ten thousand cells of [~~said~~] the tissue have a mutant nucleotide sequence.

Claims 27-31. (Canceled).